

10/049280
Rec'd PCT/PTO 31 JUL 2002



SEQUENCE LISTING

<110> BASF Aktiengesellschaft
<120> Homogentisate-Dioxygenase

<130> M/40226

<140> 19937957.2
<141> 1999-08-11

<160> 15

<170> PatentIn Ver. 2.1

<210> 1
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<212> DNA
<213> Brassica napus

<220>
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<223> /function= "restriction site"

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ctctttactg ctaaacaaga tttctctccg ttcaatgtgg ttgcctggca tggcaattac 180
gtgccttata agtatgacct gcacaagttc tgtccataca acactgtcct tgtagaccat 240
ggagatccat ctgtaaatac agttctgaca gcaccaacgg ataaacctgg tgtggccttg 300
cttgattttg tcatattccc tctcgttgg ttggttgctg agcatacctt tcgacctcct 360
tactaccatc gtaactgcat gagtgaattt atgggcctaa tctatggtgc ttacgaggcc 420
aaagctgatg gatttctacc tgggtggcgca agtcttcaca gttgtatgac acctcatggt 480
ccagatacaa ccacatacga ggcgacgatt gctcgtgtaa atgcaatggc tccttataag 540
ctcacaggca ccatggcctt catgtttgag gtacc 575

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<220>
<223> description of artificial sequence: /desc
oligonucleotide of Arabidopsis

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26

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<212> DNA
<213> artificial sequence

<220>
<223> description of artificial sequence: /desc
oligonucleotide of Arabidopsis

<220>
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<400> 3
ggtacctcra acatraangc catngtncc

29

<210> 4
<211> 25
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<220>
<223> description of artificial sequence: /desc =
amplification primer for legumin promoter

<400> 4
gaattcgatc tgctgtctca aactc

25

<210> 5
<211> 26
<212> DNA
<213> artificial sequence

<220>
<223> description of artificial sequence: /desc =
amplification primer for legumin promoter

<400> 5
ggtaccgtga tagtaaacaa ctaatg

26

<210> 6
<211> 34
<212> DNA
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<220>
<223> description of artificial sequence: /desc =
amplification primer for transit peptide from pSK-FNR

<400> 6
atggtacctt ttttgcataa acttatcttc atag

34

<210> 7
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<220>
<223> description of artificial sequence: /desc =
amplification primer for transit peptide from pSK-FNR

<400> 7
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<220>
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 <210> 9
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 <220>
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 aagcttccga tctagtaaca taga 24

 <210> 12
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 <220>
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 35S promoter sequence used for pBinAR

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<210> 13
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<220>
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<400> 13
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<210> 14
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<212> DNA
<213> artificial sequence

<220>
<223> description of artificial sequence: /desc =
4-hydroxyphenylpyruvate dioxygenase

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<221> misc_feature
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1 5 10

gct gat cct ttt cca gtt aag gga atg gat gct gtt gtt ttc gct gtt 97
Ala Asp Pro Phe Pro Val Lys Gly Met Asp Ala Val Val Phe Ala Val
15 20 25 30

gga aac gct aag caa gct gct cat tac tac tct act gct ttc gga atg 145
Gly Asn Ala Lys Gln Ala Ala His Tyr Tyr Ser Thr Ala Phe Gly Met
35 40 45

caa ctt gtt gct tac tct gga cca gaa aac gga tct aga gaa act gct 193
Gln Leu Val Ala Tyr Ser Gly Pro Glu Asn Gly Ser Arg Glu Thr Ala
50 55 60

tct tac gtt ctt act aac gga tct gct aga ttc gtt ctt act tct gtt	241
Ser Tyr Val Leu Thr Asn Gly Ser Ala Arg Phe Val Leu Thr Ser Val	
65 70 75	
att aag cca gct acc cca tgg gga cat ttc ctt gct gat cac gtt gct	289
Ile Lys Pro Ala Thr Pro Trp Gly His Phe Leu Ala Asp His Val Ala	
80 85 90	
gaa cac gga gat gga gtt gtt gat ctt gct att gaa gtt cca gat gct	337
Glu His Gly Asp Gly Val Val Asp Leu Ala Ile Glu Val Pro Asp Ala	
95 100 105 110	
aga gct gct cat gct tac gct att gaa cat gga gct aga tct gtt gct	385
Arg Ala Ala His Ala Tyr Ala Ile Glu His Gly Ala Arg Ser Val Ala	
115 120 125	
gaa cca tac gaa ctt aag gat gaa cat gga act gtt gtt ctt gct gct	433
Glu Pro Tyr Glu Leu Lys Asp Glu His Gly Thr Val Val Leu Ala Ala	
130 135 140	
att gct act tac gga aag act aga cat act ctt gtt gat aga act gga	481
Ile Ala Thr Tyr Gly Lys Thr Arg His Thr Leu Val Asp Arg Thr Gly	
145 150 155	
tac gat gga cca tac ctt cca gga tac gtt gct gct gct cca att gtt	529
Tyr Asp Gly Pro Tyr Leu Pro Gly Tyr Val Ala Ala Ala Pro Ile Val	
160 165 170	
gaa cca cca gct cat aga acc ttc caa gct att gac cat tgt gtt ggt	577
Glu Pro Pro Ala His Arg Thr Phe Gln Ala Ile Asp His Cys Val Gly	
175 180 185 190	
aac gtt gaa ctc gga aga atg aac gaa tgg gtt gga ttc tac aac aag	625
Asn Val Glu Leu Gly Arg Met Asn Glu Trp Val Gly Phe Tyr Asn Lys	
195 200 205	
gtt atg gga ttc act aac atg aag gaa ttc gtt gga gat gat att gct	673
Val Met Gly Phe Thr Asn Met Lys Glu Phe Val Gly Asp Asp Ile Ala	
210 215 220	
act gag tac tct gct ctt atg tct aag gtt gtt gct gat gga act ctt	721
Thr Glu Tyr Ser Ala Leu Met Ser Lys Val Val Ala Asp Gly Thr Leu	
225 230 235	
aag gtt aaa ttc cca att aat gaa cca gct ctt gct aag aag aag tct	769
Lys Val Lys Phe Pro Ile Asn Glu Pro Ala Leu Ala Lys Lys Lys Ser	
240 245 250	
cag att gat gaa tac ctt gag ttc tac gga gga gct gga gtt caa cat	817
Gln Ile Asp Glu Tyr Leu Glu Phe Tyr Gly Gly Ala Gly Val Gln His	
255 260 265 270	
att gct ctt aac act gga gat atc gtg gaa act gtt aga act atg aga	865
Ile Ala Leu Asn Thr Gly Asp Ile Val Glu Thr Val Arg Thr Met Arg	
275 280 285	
gct gca gga gtt caa ttc ctt gat act cca gat tct tac tac gat act	913

Ala Ala Gly Val Gln Phe Leu Asp Thr Pro Asp Ser Tyr Tyr Asp Thr	
290 295 300	
ctt ggt gaa tgg gtt gga gat act aga gtt cca gtt gat act ctt aga	961
Leu Gly Glu Trp Val Gly Asp Thr Arg Val Pro Val Asp Thr Leu Arg	
305 310 315	
gaa ctt aag att ctt gct gat aga gat gaa gat gga tac ctt ctt caa	1009
Glu Leu Lys Ile Leu Ala Asp Arg Asp Glu Asp Gly Tyr Leu Leu Gln	
320 325 330	
atc ttc act aag cca gtt caa gat aga cca act gtg ttc ttc gaa atc	1057
Ile Phe Thr Lys Pro Val Gln Asp Arg Pro Thr Val Phe Phe Glu Ile	
335 340 345 350	
att gaa aga cat gga tct atg gga ttc gga aag ggt aac ttc aag gct	1105
Ile Glu Arg His Gly Ser Met Gly Phe Gly Lys Gly Asn Phe Lys Ala	
355 360 365	
ctt ttc gaa gct att gaa aga gaa caa gag aag aga gga aac ctt tag	1153
Leu Phe Glu Ala Ile Glu Arg Glu Gln Glu Lys Arg Gly Asn Leu	
370 375 380	
gtcgac	1159

<210> 15
 <211> 381
 <212> PRT
 <213> artificial sequence

<220>
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 4-hydroxyphenylpyruvate dioxygenase

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 20 25 30
 Ala Lys Gln Ala Ala His Tyr Tyr Ser Thr Ala Phe Gly Met Gln Leu
 35 40 45
 Val Ala Tyr Ser Gly Pro Glu Asn Gly Ser Arg Glu Thr Ala Ser Tyr
 50 55 60
 Val Leu Thr Asn Gly Ser Ala Arg Phe Val Leu Thr Ser Val Ile Lys
 65 70 75 80
 Pro Ala Thr Pro Trp Gly His Phe Leu Ala Asp His Val Ala Glu His
 85 90 95
 Gly Asp Gly Val Val Asp Leu Ala Ile Glu Val Pro Asp Ala Arg Ala
 100 105 110

Ala	His	Ala	Tyr	Ala	Ile	Glu	His	Gly	Ala	Arg	Ser	Val	Ala	Glu	Pro	115	120	125
Tyr	Glu	Leu	Lys	Asp	Glu	His	Gly	Thr	Val	Val	Leu	Ala	Ala	Ile	Ala	130	135	140
Thr	Tyr	Gly	Lys	Thr	Arg	His	Thr	Leu	Val	Asp	Arg	Thr	Gly	Tyr	Asp	145	150	155
Gly	Pro	Tyr	Leu	Pro	Gly	Tyr	Val	Ala	Ala	Ala	Pro	Ile	Val	Glu	Pro	165	170	175
Pro	Ala	His	Arg	Thr	Phe	Gln	Ala	Ile	Asp	His	Cys	Val	Gly	Asn	Val	180	185	190
Glu	Leu	Gly	Arg	Met	Asn	Glu	Trp	Val	Gly	Phe	Tyr	Asn	Lys	Val	Met	195	200	205
Gly	Phe	Thr	Asn	Met	Lys	Glu	Phe	Val	Gly	Asp	Asp	Ile	Ala	Thr	Glu	210	215	220
Tyr	Ser	Ala	Leu	Met	Ser	Lys	Val	Val	Ala	Asp	Gly	Thr	Leu	Lys	Val	225	230	235
Lys	Phe	Pro	Ile	Asn	Glu	Pro	Ala	Leu	Ala	Lys	Lys	Lys	Ser	Gln	Ile	245	250	255
Asp	Glu	Tyr	Leu	Glu	Phe	Tyr	Gly	Gly	Ala	Gly	Val	Gln	His	Ile	Ala	260	265	270
Leu	Asn	Thr	Gly	Asp	Ile	Val	Glu	Thr	Val	Arg	Thr	Met	Arg	Ala	Ala	275	280	285
Gly	Val	Gln	Phe	Leu	Asp	Thr	Pro	Asp	Ser	Tyr	Tyr	Asp	Thr	Leu	Gly	290	295	300
Glu	Trp	Val	Gly	Asp	Thr	Arg	Val	Pro	Val	Asp	Thr	Leu	Arg	Glu	Leu	305	310	315
Lys	Ile	Leu	Ala	Asp	Arg	Asp	Glu	Asp	Gly	Tyr	Leu	Leu	Gln	Ile	Phe	325	330	335
Thr	Lys	Pro	Val	Gln	Asp	Arg	Pro	Thr	Val	Phe	Phe	Glu	Ile	Ile	Glu	340	345	350
Arg	His	Gly	Ser	Met	Gly	Phe	Gly	Lys	Gly	Asn	Phe	Lys	Ala	Leu	Phe	355	360	365
Glu	Ala	Ile	Glu	Arg	Glu	Gln	Glu	Lys	Arg	Gly	Asn	Leu				370	375	380